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OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/828,217

DATE: 06/08/2001

TIME: 14:47:04

Input Set : C:\PAOLA\09828217.txt

Output Set: N:\CRF3\06082001\I828217.raw

SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: HIRANO, TOSHIO
7 KAISHO, TSUNEYASU
9 (ii) TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING
10 PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF
12 (iii) NUMBER OF SEQUENCES: 2
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
16 P.C.
17 (B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
18 (C) CITY: ARLINGTON
19 (D) STATE: VA
20 (E) COUNTRY: USA
21 (F) ZIP: 22202
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/828,217
C--> 31 (B) FILING DATE: 09-Apr-2001
32 (C) CLASSIFICATION:
41 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 09/182,563
36 (B) FILING DATE:
38 (A) APPLICATION NUMBER: PCT/JP94/01732
39 (B) FILING DATE: 14-OCT-1994
42 (A) APPLICATION NUMBER: JP 5-281622
43 (B) FILING DATE: 15-OCT-1993
45 (viii) ATTORNEY/AGENT INFORMATION:
46 (A) NAME: OBLON, NORMAN F.
47 (B) REGISTRATION NUMBER: 24,618
48 (C) REFERENCE/DOCKET NUMBER: 7625-001-0 PCT
50 (ix) TELECOMMUNICATION INFORMATION:
51 (A) TELEPHONE: 703-413-3000
52 (B) TELEFAX: 703-413-2220
55 (2) INFORMATION FOR SEQ ID NO: 1:
57 (i) SEQUENCE CHARACTERISTICS:
58 (A) LENGTH: 180 amino acids
59 (B) TYPE: amino acid
60 (C) STRANDEDNESS: single
61 (D) TOPOLOGY: linear
63 (ii) MOLECULE TYPE: peptide
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70 Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly

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71      1              5              10              15
73  Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
74              20              25              30
76  Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
77              35              40              45
79  Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
80              50              55              60
82  Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
83      65              70              75              80
85  Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
86              85              90              95
88  Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
89              100             105             110
91  Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
92              115             120             125
94  Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
95      130             135             140
97  Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
98      145             150             155             160
100  Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
101              165             170             175
103  Ala Leu Leu Gln
104              180

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 996 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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121 GTGGAATTCA TGGCATCTAC TTCGTATGAC TATTGCAGAG TGCCCATGGA AGACGGGGGAT      60
123 AAGCGCTGTA AGCTTCTGCT GGGGATAGGA ATTCTGGTGC TCCTGATCAT CGTGATTCTG      120
125 GGGGTGCCCT TGATTATCTT CACCATCAAG GCCAACAGCG AGGCCTGCCG GGACGGCCTT      180
127 CGGGCAGTGA TGGAGTGTCG CAATGTCACC CATCTCCTGC AACAAGAGCT GACCGAGGCC      240
129 CAGAAGGGCT TTCAGGATGT GGAGGCCCAG GCCGCCACCT GCAACCACAC TGTGATGGCC      300
131 CTAATGGCTT CCCTGGATGC AGAGAAGGCC CAAGGACAAA AGAAAGTGGA GGAGCTTGAG      360
133 GGAGAGATCA CTACATTAAA CCATAAGCTT CAGGACGCGT CTGCAGAGGT GGAGCGACTG      420
135 AGAAGAGAAA ACCAGGTCTT AAGCGTGAGA ATCGCGGACA AGAAGTACTA CCCCAGCTCC      480
137 CAGGACTCCA GTCCTGCTGC GCGGCCCCAG CTGCTGATTG TGCTGCTGGG CCTCAGCGCT      540
139 CTGCTGCAGT GAGATCCCAG GAAGCTGGCA CATCTTGGA GGTCCGTCCT GCTCGGCTTT      600
141 TCGCTTGAAC ATTCCCTTGA TCTCATCAGT TCTGAGCGGG TCATGGGGCA ACACGGTTAG      660
143 CGGGGAGAGC ACGGGGTAGC CGGAGAAGGG CCTCTGGAGC AGGTCTGGAG GGGCCATGGG      720
145 GCAGTCCTGG GTGTGGGGAC ACAGTCGGGT TGACCCAGGG CTGTCTCCCT CCAGAGCCTC      780
147 CCTCCGGACA ATGAGTCCCC CCTCTTGCTT CCCACCCTGA GATTGGGCAT GGGGTGCGGT      840
149 GTGGGGGGCA TGTGCTGCCT GTTGTATG GTTTTTTT CGGGGGGGT TGCTTTTTTC      900
151 TGGGGTCTTT GAGCTCCAAA AAATAAACAC TTCCTTTGAG GGAGAGCAAA AAAAAAAAAA      960
153 AAAAAAAAAA AAAAAAAAAA AAAGAATTCC ACCACA                                996

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VERIFICATION SUMMARY

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]